

SEQUENCE LISTING

<110> MIYAWAKI, ATSUSHI
 TSUTSUI, HIDEKAZU
 KARASAWA, SATOSHI

<120> FLUORESCENT PROTEIN AND CHROMOPROTEIN

<130> P28993

<140> 10/561,041

<141> 2005-12-16

<150> PCT/JP04/08786

<151> 2004-06-16

<150> JP 2003-170324

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<170> PatentIn Ver. 3.3

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<213> Montipora sp.

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 35 40 45

Glu Lys Gly Gly Pro Leu Pro Phe Ser Val Asp Ile Leu Ser Ala Ala
 50 55 60

Phe Leu Tyr Gly Asn Arg Cys Met Thr Lys Tyr Pro Gly Gly Ile Val
 65 70 75 80
 Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Glu Arg Ser
 85 90 95
 Phe Leu Phe Glu Asp Gly Ala Val Cys Thr Ala Ser Ala Asp Ile Arg
 100 105 110
 Leu Ser Val Glu Asp Asn Cys Phe Tyr His Glu Ser Lys Phe Ser Gly
 115 120 125
 Val Asn Phe Pro Val Asp Gly Pro Val Met Thr Leu Ala Thr Thr Gly
 130 135 140
 Trp Glu Pro Ser Ser Glu Lys Met Val Pro Ser Gly Gly Ile Val Lys
 145 150 155 160
 Gly Asp Val Thr Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr Arg
 165 170 175
 Cys Gln Phe Asn Ser Asn Tyr Lys Ala Lys Thr Glu Pro Lys Glu Met
 180 185 190
 Pro Asp Phe His Phe Val Glu His Lys Ile Val Arg Thr Asp Leu Gly
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 His Met Glu Gly Cys Val Asn Gly His Glu Phe Thr Ile Lys Gly Glu
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 Gly Thr Gly Gln Pro Tyr Glu Gly Thr Gln Cys Ile Gln Leu Arg Val
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Glu Lys Gly Gly Pro Leu Pro Phe Ser Val Asp Ile Leu Ser Ala Ala	
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Phe Leu Tyr Gly Asn Arg Cys Met Thr Lys Tyr Pro Gly Gly Ile Val	
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gac tat ttc aag aac tca tgc cct gct gga tat aca tgg gaa agg tct	288
Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Glu Arg Ser	
85 90 95	
ttt ctc ttt gaa gat ggc gcg gtg tgc aca gca agt gca gat ata cgc	336
Phe Leu Phe Glu Asp Gly Ala Val Cys Thr Ala Ser Ala Asp Ile Arg	
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Leu Ser Val Glu Asp Asn Cys Phe Tyr His Glu Ser Lys Phe Ser Gly	
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Val Asn Phe Pro Val Asp Gly Pro Val Met Thr Leu Ala Thr Thr Gly	
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tgg gag cca tcc tcc gag aaa atg gtg ccc agt ggg ggg ata gtg aaa	480
Trp Glu Pro Ser Ser Glu Lys Met Val Pro Ser Gly Gly Ile Val Lys	
145 150 155 160	
ggg gat gtc acc atg tac ctc ctt ctg aag gat ggt ggg cgt tac cgg	528
Gly Asp Val Thr Met Tyr Leu Leu Leu Lys Asp Gly Gly Arg Tyr Arg	
165 170 175	
tgc cag ttc aac agt aat tac aag gca aag act gag ccg aaa gag atg	576
Cys Gln Phe Asn Ser Asn Tyr Lys Ala Lys Thr Glu Pro Lys Glu Met	
180 185 190	
cca gac ttt cac ttc gtg gag cat aag atc gta agg acc gac ctc ggt	624
Pro Asp Phe His Phe Val Glu His Lys Ile Val Arg Thr Asp Leu Gly	
195 200 205	
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 35 40 45
 Ile Ile Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
 50 55 60
 Ser Ser Val Phe His Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala
 65 70 75 80
 Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
 85 90 95
 Glu Arg Ser Phe Leu Phe Glu Asp Gly Ala Val Ala Thr Ala Ser Trp
 100 105 110
 Asn Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Phe His
 115 120 125
 Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
 130 135 140
 Asp Trp Glu Lys Ser Phe Glu Lys Met Thr Val Ser Lys Glu Val Leu
 145 150 155 160
 Arg Gly Asp Val Thr Met Phe Leu Met Leu Glu Gly Gly Gly Ser His
 165 170 175
 Arg Cys Gln Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met
 180 185 190
 Pro Pro Asn His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
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<222> (1)..(696)

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atc atc aag cct gcg gga aaa ccc ctt cca ttc tcc ttt gac ata ctg Ile Ile Lys Pro Ala Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu 50 55 60	192
tca tca gtc ttt cat tat gga aac agg tgc ttc aca aag tac cct gca Ser Ser Val Phe His Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala 65 70 75 80	240
gac atg cct gac tat ttc aag caa gca ttc cca gat gga atg tcg tat Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr 85 90 95	288
gaa agg tca ttt cta ttt gaa gat gga gca gtt gct aca gcc agc tgg Glu Arg Ser Phe Leu Phe Glu Asp Gly Ala Val Ala Thr Ala Ser Trp 100 105 110	336
aac att cgt ctc gaa gga aat tgc ttc atc cac aat tcc atc ttt cat Asn Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Phe His 115 120 125	384
ggc gta aac ttt ccc gct gat gga ccc gta atg aaa aag cag aca att Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile 130 135 140	432
gac tgg gag aag tcc ttc gaa aaa atg act gtg tct aaa gag gtg cta Asp Trp Glu Lys Ser Phe Glu Lys Met Thr Val Ser Lys Glu Val Leu 145 150 155 160	480
aga ggt gat gtg act atg ttt ctt atg ctc gaa gga ggt ggt tct cac Arg Gly Asp Val Thr Met Phe Leu Met Leu Glu Gly Gly Gly Ser His 165 170 175	528
aga tgc cag ttt cac tcc act tac aaa aca gag aag ccg gtc gca atg Arg Cys Gln Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met 180 185 190	576
ccc ccg aat cat gtc gta gaa cat caa att gtg agg acc gac ctt ggc Pro Pro Asn His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly 195 200 205	624
caa agt gca aaa ggc ttt aca gtc aag ctg gaa gca cat gct gtg gct Gln Ser Ala Lys Gly Phe Thr Val Lys Leu Glu Ala His Ala Val Ala 210 215 220	672
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 Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
 50 55 60
 Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala
 65 70 75 80
 Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
 85 90 95
 Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp
 100 105 110
 Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His
 115 120 125
 Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
 130 135 140
 Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu
 145 150 155 160
 Arg Gly Asp Val Thr Gln Phe Leu Leu Leu Glu Gly Gly Gly Tyr Gln
 165 170 175
 Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met
 180 185 190
 Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
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gta gga act gga aac cct tac gaa ggg aaa cag atg tcc gaa tta gtg	144
Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val	
35 40 45	
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Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu	
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Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala	
65 70 75 80	
gac atg cct gac tat ttc aag caa gca ttc cca gat gga atg tca tat	288
Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr	
85 90 95	
gaa agg tca ttt cta ttt gag gat gga gga gtt gct aca gcc agc tgg	336
Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp	
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agc att cgt ctc gaa gga aat tgc ttc atc cac aat tcc atc tat cat	384
Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His	
115 120 125	
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ggc tgg gat aag tcc ttc gaa aaa atg agt gtg gct aaa gag gtg cta	480
Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu	
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aga ggt gat gtg act cag ttt ctt ctg ctc gaa gga ggt ggt tac cag	528
Arg Gly Asp Val Thr Gln Phe Leu Leu Glu Gly Gly Gly Tyr Gln	
165 170 175	
aga tgc cgg ttt cac tcc act tac aaa acg gag aag cca gtc gca atg	576
Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met	
180 185 190	
ccc ccg agt cat gtc gta gaa cat caa att gtg agg acc gac ctt ggc	624
Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly	
195 200 205	

caa act gca aaa ggc ttc aag gtc aag ctg gaa gaa cat gct gag gct 672
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 35 40 45
 Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
 50 55 60
 Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala
 65 70 75 80
 Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
 85 90 95
 Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp
 100 105 110
 Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His
 115 120 125
 Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
 130 135 140
 Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu
 145 150 155 160
 Arg Gly Asp Val Thr His Phe Leu Leu Leu Glu Gly Gly Gly Tyr Gln
 165 170 175
 Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met
 180 185 190
 Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
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His Val Asn Pro Leu Lys Val Lys
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Tyr Arg Met Glu Gly Ser Val Asn Gly His Glu Phe Thr Ile Glu Gly
20 25 30
gta gga act gga aac cct tac gaa ggg aaa cag atg tcc gaa tta gtg 144
Val Gly Thr Gly Asn Pro Tyr Glu Gly Lys Gln Met Ser Glu Leu Val
35 40 45
atc atc aag tct aag gga aaa ccc ctt cca ttc tcc ttt gac ata ctg 192
Ile Ile Lys Ser Lys Gly Lys Pro Leu Pro Phe Ser Phe Asp Ile Leu
50 55 60
tca aca gcc ttt caa tat gga aac aga tgc ttc aca aag tac cct gca 240
Ser Thr Ala Phe Gln Tyr Gly Asn Arg Cys Phe Thr Lys Tyr Pro Ala
65 70 75 80
gac atg cct gac tat ttc aag caa gca ttc cca gat gga atg tca tat 288
Asp Met Pro Asp Tyr Phe Lys Gln Ala Phe Pro Asp Gly Met Ser Tyr
85 90 95
gaa agg tca ttt cta ttt gag gat gga gga gtt gct aca gcc agc tgg 336
Glu Arg Ser Phe Leu Phe Glu Asp Gly Gly Val Ala Thr Ala Ser Trp
100 105 110
agc att cgt ctc gaa gga aat tgc ttc atc cac aat tcc atc tat cat 384
Ser Ile Arg Leu Glu Gly Asn Cys Phe Ile His Asn Ser Ile Tyr His
115 120 125
ggc gta aac ttt ccc gct gat gga ccc gta atg aag aag cag aca att 432
Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Gln Thr Ile
130 135 140
ggc tgg gat aag tcc ttc gaa aaa atg agt gtg gct aaa gag gtg cta 480
Gly Trp Asp Lys Ser Phe Glu Lys Met Ser Val Ala Lys Glu Val Leu
145 150 155 160
aga ggt gat gtg act cat ttt ctt ctg ctc gaa gga ggt ggt tac cag 528
Arg Gly Asp Val Thr His Phe Leu Leu Leu Glu Gly Gly Gly Tyr Gln
165 170 175

aga tgc cgg ttt cac tcc act tac aaa acg gag aag cca gtc gca atg 576
 Arg Cys Arg Phe His Ser Thr Tyr Lys Thr Glu Lys Pro Val Ala Met
 180 185 190

ccc ccg agt cat gtc gta gaa cat caa att gtg agg acc gac ctt ggc 624
 Pro Pro Ser His Val Val Glu His Gln Ile Val Arg Thr Asp Leu Gly
 195 200 205

caa act gca aaa ggc ttc aag gtc aag ctg gaa gaa cat gct gag gct 672
 Gln Thr Ala Lys Gly Phe Lys Val Lys Leu Glu Glu His Ala Glu Ala
 210 215 220

cat gtt aac cct ttg aag gtt aaa taa 699
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Gly Ile Gly Asp Pro Phe Glu Gly Lys Gln Thr Ser Ile Asp Leu Cys
 35 40 45

Val Val Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala
 50 55 60

Val Phe Asp Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Gln Asp Leu
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Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gln Arg
 85 90 95

Ser Phe Leu Phe Glu Asp Gly Ala Val Cys Thr Ala Ser Ala Asp Ile
 100 105 110

Arg Val Ser Val Glu Glu Asn Cys Phe Tyr His Glu Ser Lys Phe His
 115 120 125

Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr
 130 135 140

Asn Trp Glu Pro Ser Cys Glu Lys Ile Thr Pro Ile Leu Asn Glu Gly
 145 150 155 160

Ile Leu Lys Gly Asp Val Thr Met Phe Leu Leu Leu Lys Asp Gly Gly
 165 170 175

Arg Tyr Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ala Asp Ala
 180 185 190

Lys Lys Met Pro Glu Trp His Phe Ile Gln His Lys Leu Thr Arg Glu
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Ile Ala Tyr Arg Ser Thr Leu Pro
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 Arg Met Glu Gly Cys Val Asp Gly His Lys Phe Val Ile Thr Gly Asp
 20 25 30

ggc att gga gat cct ttc gaa ggg aaa cag act agt att gat ctg tgt 144
 Gly Ile Gly Asp Pro Phe Glu Gly Lys Gln Thr Ser Ile Asp Leu Cys
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gtg gtt gaa ggg gga cca ctg cca ttc tcc gaa gat ata ttg tct gct 192
 Val Val Glu Gly Gly Pro Leu Pro Phe Ser Glu Asp Ile Leu Ser Ala
 50 55 60

gtg ttt gac tac gga aac agg gtc ttt act aaa tat cct caa gac ctt 240
 Val Phe Asp Tyr Gly Asn Arg Val Phe Thr Lys Tyr Pro Gln Asp Leu
 65 70 75 80

gtt gac tat ttc aag aac tca tgt cct gct gga tat aca tgg caa agg 288
 Val Asp Tyr Phe Lys Asn Ser Cys Pro Ala Gly Tyr Thr Trp Gln Arg
 85 90 95

tct ttt ctc ttt gaa gat ggt gca gtt tgc aca gcc agt gca gat ata 336
 Ser Phe Leu Phe Glu Asp Gly Ala Val Cys Thr Ala Ser Ala Asp Ile
 100 105 110

aga gtg agt gtt gag gag aac tgc ttt tat cac gag tcc aag ttt cat 384
 Arg Val Ser Val Glu Glu Asn Cys Phe Tyr His Glu Ser Lys Phe His
 115 120 125

gga gtg aac ttt cct gct gat gga cct gtg atg aaa aag atg aca act 432
 Gly Val Asn Phe Pro Ala Asp Gly Pro Val Met Lys Lys Met Thr Thr
 130 135 140

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 Asn Trp Glu Pro Ser Cys Glu Lys Ile Thr Pro Ile Leu Asn Glu Gly
 145 150 155 160
 ata ttg aaa gga gat gtc acc atg ttc ctc ctt ctg aag gat ggt ggg 528
 Ile Leu Lys Gly Asp Val Thr Met Phe Leu Leu Leu Lys Asp Gly Gly
 165 170 175
 cgt tac cgg tgc cag ttc gac aca gtt tac aaa gca aag gct gac gca 576
 Arg Tyr Arg Cys Gln Phe Asp Thr Val Tyr Lys Ala Lys Ala Asp Ala
 180 185 190
 aaa aag atg ccg gaa tgg cac ttc atc caa cat aag ctc acc cgg gaa 624
 Lys Lys Met Pro Glu Trp His Phe Ile Gln His Lys Leu Thr Arg Glu
 195 200 205
 gac cgc agc gat gct aag cac cag aaa tgg cga ctg gta gaa aat gct 672
 Asp Arg Ser Asp Ala Lys His Gln Lys Trp Arg Leu Val Glu Asn Ala
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 Ile Ala Tyr Arg Ser Thr Leu Pro
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 35 40 45
 Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Ala Pro Cys Cys Met Tyr
 50 55 60
 Gly Ser Lys Thr Phe Ile Lys His Val Ser Gly Ile Pro Asp Tyr Phe
 65 70 75 80
 Lys Asp Ser Leu Pro Glu Gly Tyr Thr Trp Glu Arg Thr Gln Ile Tyr
 85 90 95
 Glu Asp Gly Gly Tyr Leu Thr Ile His Gln Asp Thr Ser Ile Gln Gly
 100 105 110
 Asp Ser Phe Ile Phe Lys Val Lys Val Ile Gly Ala Asn Phe Pro Ala
 115 120 125
 Asn Gly Pro Val Met Gln Lys Lys Thr Ala Gly Trp Glu Pro Cys Val
 130 135 140

Glu Met Leu Tyr Pro Arg Asp Gly Val Leu Cys Gly Gln Ser Leu Met
 145 150 155 160
 Ala Leu Lys Cys Thr Asp Gly Asn His Leu Thr Ser His Leu Arg Thr
 165 170 175
 Thr Tyr Arg Ser Arg Lys Pro Ala Asn Ala Val Asn Met Pro Lys Phe
 180 185 190
 His Phe Gly Asp His Arg Ile Glu Ile Leu Lys Glu Ala Glu Pro Gly
 195 200 205
 Lys Phe Tyr Glu Gln Tyr Glu Ser Ala Val Ala Arg Tyr Cys Glu Ala
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 Ala Pro Ser Lys Leu Gly His His
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 20 25 30
 aag cca ttt gaa ggt acc cag gag gaa aag ata aga atc act gaa gga 144
 Lys Pro Phe Glu Gly Thr Gln Glu Glu Lys Ile Arg Ile Thr Glu Gly
 35 40 45
 ggt ccc tta cca ttt gcg tac gat att ttg gca cct tgt tgc atg tat 192
 Gly Pro Leu Pro Phe Ala Tyr Asp Ile Leu Ala Pro Cys Cys Met Tyr
 50 55 60
 gga agc aaa acc ttc atc aag cat gtc tca ggg att cca gat tac ttc 240
 Gly Ser Lys Thr Phe Ile Lys His Val Ser Gly Ile Pro Asp Tyr Phe
 65 70 75 80
 aag gat tct tta cct gaa gga tac act tgg gaa aga acc caa atc tac 288
 Lys Asp Ser Leu Pro Glu Gly Tyr Thr Trp Glu Arg Thr Gln Ile Tyr
 85 90 95
 gag gat gga ggc tat ctt acc att cac cag gac aca agc ata cag gga 336
 Glu Asp Gly Gly Tyr Leu Thr Ile His Gln Asp Thr Ser Ile Gln Gly
 100 105 110

gat agc ttt att ttc aag gtt aaa gtc atc ggt gcc aac ttc cct gcc 384
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115 120 125

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130 135 140

gag atg ctt tat cca cgt gac gga gtc ctg tgt ggg cag tcc ttg atg 480
Glu Met Leu Tyr Pro Arg Asp Gly Val Leu Cys Gly Gln Ser Leu Met
145 150 155 160

gcc ctg aaa tgc act gat ggt aac cat ttg acg agc cat ctg cga act 528
Ala Leu Lys Cys Thr Asp Gly Asn His Leu Thr Ser His Leu Arg Thr
165 170 175

act tac agg tcc aga aag cca gcc aat gcg gtt aat atg cca aaa ttt 576
Thr Tyr Arg Ser Arg Lys Pro Ala Asn Ala Val Asn Met Pro Lys Phe
180 185 190

cat ttt gga gac cat cgc att gag ata cta aag gaa gca gaa cca ggc 624
His Phe Gly Asp His Arg Ile Glu Ile Leu Lys Glu Ala Glu Pro Gly
195 200 205

aag ttt tat gaa cag tac gaa tca gca gtg gcc agg tac tgt gaa gct 672
Lys Phe Tyr Glu Gln Tyr Glu Ser Ala Val Ala Arg Tyr Cys Glu Ala
210 215 220

gca cca tca aag ctt gga cat cac taa 699
Ala Pro Ser Lys Leu Gly His His
225 230

<210> 13
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<213> Lobophytum crassum

<400> 13
Met Ser Val Ile Lys Gln Glu Met Lys Ile Lys Leu His Met Glu Gly
1 5 10 15

Asn Val Asn Gly His Ala Phe Val Ile Glu Gly Asp Gly Lys Gly Lys
20 25 30

Pro Tyr Asp Gly Thr Gln Thr Leu Asn Leu Thr Val Lys Glu Gly Ala
35 40 45

Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Asn Ala Phe Gln Tyr Gly
50 55 60

Asn Arg Ala Phe Thr Lys Tyr Pro Ala Asp Ile Pro Asp Tyr Phe Lys
65 70 75 80

Gln Thr Phe Pro Glu Gly Tyr Ser Trp Glu Arg Thr Met Ser Tyr Glu
85 90 95

Asp Asn Ala Ile Cys Asn Val Arg Ser Glu Ile Ser Met Glu Gly Asp
 100 105 110

Cys Phe Ile Tyr Lys Ile Arg Phe Asp Gly Lys Asn Phe Pro Pro Asn
 115 120 125

Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu
 130 135 140

Met Met Tyr Val Arg Asp Gly Phe Leu Met Gly Asp Val Asn Met Ala
 145 150 155 160

Leu Leu Leu Glu Gly Gly Gly His His Arg Cys Asp Phe Lys Thr Ser
 165 170 175

Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His Tyr Val Asp
 180 185 190

His Arg Ile Glu Ile Leu Ser His Asp Arg Asp Tyr Ser Lys Val Lys
 195 200 205

Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Leu Leu Pro Ser Gln Ala
 210 215 220

<210> 14
 <211> 675
 <212> DNA
 <213> Lobophytum crassum

<220>
 <221> CDS
 <222> (1)..(672)

<400> 14
 atg agt gtg att aaa caa gaa atg aag atc aag ctg cat atg gaa gga 48
 Met Ser Val Ile Lys Gln Glu Met Lys Ile Lys Leu His Met Glu Gly
 1 5 10 15

aat gta aac ggt cat gca ttt gtg att gaa gga gat gga aaa gga aag 96
 Asn Val Asn Gly His Ala Phe Val Ile Glu Gly Asp Gly Lys Gly Lys
 20 25 30

cct tac gat ggg aca cag act tta aac ctg aca gtg aaa gaa ggc gca 144
 Pro Tyr Asp Gly Thr Gln Thr Leu Asn Leu Thr Val Lys Glu Gly Ala
 35 40 45

cct ctc cct ttt tct tac gac atc ttg aca aat gcg ttc cag tac gga 192
 Pro Leu Pro Phe Ser Tyr Asp Ile Leu Thr Asn Ala Phe Gln Tyr Gly
 50 55 60

aat aga gca ttc act aaa tat cca gcc gat ata cca gac tat ttc aag 240
 Asn Arg Ala Phe Thr Lys Tyr Pro Ala Asp Ile Pro Asp Tyr Phe Lys
 65 70 75 80

cag acg ttt ccc gag ggg tat tca tgg gaa aga acc atg agt tat gaa 288
 Gln Thr Phe Pro Glu Gly Tyr Ser Trp Glu Arg Thr Met Ser Tyr Glu
 85 90 95

gac aac gcc att tgc aac gtg aga agc gag atc agc atg gaa ggc gac	336
Asp Asn Ala Ile Cys Asn Val Arg Ser Glu Ile Ser Met Glu Gly Asp	
100 105 110	
tgc ttt atc tat aaa att cgg ttt gat ggc aag aac ttt ccc ccc aat	384
Cys Phe Ile Tyr Lys Ile Arg Phe Asp Gly Lys Asn Phe Pro Pro Asn	
115 120 125	
ggt cca gtt atg cag aag aaa act ttg aag tgg gaa cca tcc act gag	432
Gly Pro Val Met Gln Lys Lys Thr Leu Lys Trp Glu Pro Ser Thr Glu	
130 135 140	
atg atg tac gtg cgt gat ggg ttt ctg atg ggt gat gtt aac atg gct	480
Met Met Tyr Val Arg Asp Gly Phe Leu Met Gly Asp Val Asn Met Ala	
145 150 155 160	
ctg ttg ctt gaa gga ggt ggc cat cac cga tgt gac ttc aaa act tcc	528
Leu Leu Leu Glu Gly Gly Gly His His Arg Cys Asp Phe Lys Thr Ser	
165 170 175	
tac aaa gcg aaa aag gtt gtg cag ttg cca gat tat cac tat gtg gac	576
Tyr Lys Ala Lys Lys Val Val Gln Leu Pro Asp Tyr His Tyr Val Asp	
180 185 190	
cat cgt atc gag atc ttg agc cat gac agg gat tac agc aaa gtc aag	624
His Arg Ile Glu Ile Leu Ser His Asp Arg Asp Tyr Ser Lys Val Lys	
195 200 205	
ctg tat gag aat gcg gtt gct cgc tat tct ttg ctg cca agt cag gcc	672
Leu Tyr Glu Asn Ala Val Ala Arg Tyr Ser Leu Leu Pro Ser Gln Ala	
210 215 220	
tag	675

<210> 15

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 15

gaaggrtgyg tcaayggrca y

21

<210> 16

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 16
acvggdccat ydgvaagaaa rtt

23

<210> 17
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<220>
<221> modified_base
<222> (24)..(25)
<223> inosine

<220>
<221> modified_base
<222> (29)..(30)
<223> inosine

<220>
<221> modified_base
<222> (34)..(35)
<223> inosine

<400> 17
ggccacgcgt cgactagtac gggnnngggnn gggnnng

36

<210> 18
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 18
ccatcttcaa agagaaaaga ccttt

25

<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19
ggccacgcgt cgactagtac

20

<210> 20
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 20
 catgagttct tgaaatagtc aac

23

<210> 21
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 21
 atggctcttt caaagcgagg tg

22

<210> 22
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 22
 gggggatccg accatggctc tttcaaagcg aggtg

35

<210> 23
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 23
 tagaaatgac ctttcatatg acattc

26

<210> 24
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 24

tctgtttcca tattgaaagg ctg

23

<210> 25

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 25

atgggtgtctt attcaaagca aggcacgcga ca

32

<210> 26

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 26

cgggatccga ccatggtgtc ttattcaaag caaggcatcg caca

44

<210> 27

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 27

tagaaatgac ctttcatatg acattc

26

<210> 28

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 28

tctgtttcca tattgaaagg ctg

23

<210> 29
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 29
atggtgtctt attcaaagca aggcacgca ca 32

<210> 30
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 30
cgggatccga ccatggtgtc ttattcaaag caaggcatcg caca 44

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 31
atggctcttt caaagcacgg tc 22

<210> 32
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 32
gggggatccg accatggctc tttcaaagca cggtc 35

<210> 33
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<220>
 <221> modified_base
 <222> (3)
 <223> inosine

<220>
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 <222> (9)
 <223> inosine

<220>
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 <222> (21)
 <223> a, c, g, t, unknown or other

<400> 33
 ggnwsbgtna ayggvcayda ntt

23

<210> 34
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<220>
 <221> modified_base
 <222> (4)
 <223> inosine

<220>
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 <222> (15)
 <223> inosine

<220>
 <221> modified_base
 <222> (18)
 <223> inosine

<220>
 <221> modified_base
 <222> (21)
 <223> inosine

<400> 34
 gtctntcttyt gcacnacngg nccatydgva ggaaa

35

<210> 35
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 35
 ccttgaaaat aaagctatct

20

<210> 36
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 36
 ccctgtatgc ttgtgtcctg

20

<210> 37
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 37
 cccgatccg accatgggtg cttcattggt taagaa

36

<210> 38
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<220>
 <221> modified_base
 <222> (7)
 <223> inosine

<400> 38
 grraggnwsb gthaayggvc a

21

<210> 39
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 39
 aactggaaga attcgcggcc gcaggaa

27

<210> 40
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<220>
 <221> modified_base
 <222> (4)
 <223> inosine

<220>
 <221> modified_base
 <222> (15)
 <223> inosine

<220>
 <221> modified_base
 <222> (18)
 <223> inosine

<220>
 <221> modified_base
 <222> (21)
 <223> inosine

<400> 40
 gtcntcttyt gcacnacngg nccatydgva ggaaa

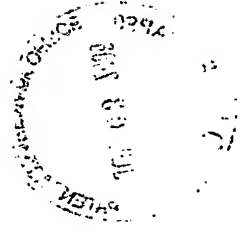
35

<210> 41
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 41
 ttgtcaagat atcgaaagcg aacggcagag

30



<210> 42
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 42
ggccacgcgt cgactagtac

20

<210> 43
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 43
cttctcacgt tgcaaatggc

20

<210> 44
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 44
cccggatccg atgagtgtga ttacawcaga aatgaagatg gagc

44